

**In the claims:**

1. (Currently amended) A method for determining the prognosis of a patient with breast cancer, the method comprising assigning a prognosis to the patient by obtaining an based on the expression profile levels of nucleic acid ~~expression~~ products of a prognostic set of genes from in a breast tumor of said patient, comparing the expression profile under test with a previously determined standard expression signature profile which is associated with low or high NPI, wherein the prognostic set of nucleic acid products comprises includes adenine phosphoribosyltransferase (SEQ ID NO: 1), MCM4 minichromosome maintenance deficient 4 (S. cerevisiae) (SEQ ID NOS: 2-5, exonuclease 1 (SEQ ID NOS: 6-11), Metallothionein 1H-like protein (SEQ ID NO: 12), and clone IMAGE:5270727 (SEQ ID NO:13), and wherein a patient having higher levels of nucleic acid expression products encoding of adenine phosphoribosyltransferase, MCM4 minichromosome maintenance deficient 4 (S. cerevisiae), exonuclease 1, Metallothionein 1H-like protein, and clone IMAGE:5270727 in said expression profile has a poorer prognosis as determined by comparison with said previously determined standard expression signature profile, said method optionally comprising the step of determining least one status selected from the group consisting of estrogen receptor (ER) status and Erb2 status of the tumour sample.

2. (Currently amended) The method of claim 1, wherein the prognostic set comprises at least 10, 20, 30, 40, 50, 60 or all of the ~~genes~~ nucleic acids encoded by SEQ ID NOS: 1-309 of Table S6.

Claims 3 and 4 (Cancelled)

5. (Currently Amended) The method of claim 1 comprising the



steps of:

(a) obtaining a breast tumour sample from the patient;  
and

(b) measuring the levels of said nucleic acid expression products in the sample of the genes of the prognostic set, thereby obtaining an expression profile.

6. (Previously presented) The method of claim 5 wherein step (b) comprises contacting said nucleic acid expression products obtained from the sample with a plurality of binding members capable of binding to said nucleic acid expression products, wherein such binding may be measured.

Claim 7 (Previously presented): The method of claim 6 wherein the binding members are complementary nucleic acid sequences.

Claim 8 (Currently Amended): The method of claim 1, comprising classifying the sample of breast tumour as being of either high Nottingham Prognostic Index (NPI) or low, or as either of good or bad prognosis NPI relative to a previously determined NPI expression signature profile, wherein an upregulation of the nucleic acid expression products of adenine phosphoribosyltransferase, MCM4 minichromosome maintenance deficient 4 (*S. cerevisiae*), exonuclease 1, Metallothionein 1H-like protein, and clone IMAGE: 5270727 is indicative of a poor prognosis or high NPI, and wherein a downregulation of the nucleic acid expression products of adenine phosphoribosyltransferase, MCM4 minichromosome maintenance deficient 4 (*S. cerevisiae*), exonuclease 1, Metallothionein 1H-like protein, and clone IMAGE: 5270727 is indicative of a good prognosis or low NPI.

Claim 9 (Cancelled)

Claim 10 (Previously presented): The method of claim 9 wherein the previously obtained profiles are stored as a database of



profiles.

Claim 11 (Previously presented): The method of claim 1 further comprising comparing the expression levels of the prognostic set in the breast tumour sample before and after treatment to detect a change in the expression profile indicative of an improved prognosis or worsened prognosis.

Claim 12 (Currently Amended): An apparatus for assigning a prognosis to a breast tumour sample, which apparatus comprises a solid support to which are attached a plurality of nucleic acid binding members, each binding member being capable of specifically and independently binding to an expression product of one of a prognostic set of genes, wherein the prognostic set includes adenine phosphoribosyltransferase (SEQ ID NO: 1), MCM4 minichromosome maintenance deficient 4 (*S. cerevisiae*) (SEQ ID NOS: 2-5), exonuclease 1 (SEQ ID NOS: 6-11), Metallothionein 1H-like protein (SEQ ID NO: 12), and clone IMAGE: 5270727 (SEQ ID NO: 13), and wherein said solid support houses nucleic acid binding members for not more than 500 different genes.

Claim 13 (Currently Amended): The apparatus of claim 12, wherein the prognostic set comprises at least 5, 10, 20, 30, 40, 50, 60 or all of the ~~genes~~ nucleic acids encoded by SEQ ID NOS: 1- 309~~of Table S6~~.

Claim 14 (Currently Amended): The apparatus of claim 12 wherein the solid support has attached thereto only binding members that are capable of specifically and independently binding to expression products of the ~~genes~~ nucleic acids encoded by SEQ ID NOS: 1- 309 ~~of Table S6~~.

Claim 15 (Cancelled)

Claim 16 (Currently Amended): A kit for assigning a prognosis



to a patient with breast cancer, said kit comprising a plurality of nucleic acid binding members capable of specifically binding to nucleic acid expression products of genes of a prognostic set of genes and a detection reagent, wherein the prognostic set includes adenine phosphoribosyltransferase (SEQ ID NO: 1), MCM4 minichromosome maintenance deficient 4 (*S. cerevisiae*) (SEQ ID NOS: 2-5, exonuclease 1 (SEQ ID NOS: 6-11), Metallothionein 1H-like protein (SEQ ID NO: 12), and clone IMAGE:5270727 (SEQ ID NO:13), wherein said kit optionally comprises the apparatus of claim 12 and comprises less than 500 binding members.

Claim 17 (Currently amended): The kit of claim 16, wherein the prognostic set comprises at least 10, 20, 30, 40, 50, 60 or all of nucleic acids encoded by SEQ ID NOS:1-309 ~~the genes of Table S6.~~

Claim 18 (Previously presented): The kit of claim 16, further comprising a data analysis tool, wherein the data analysis tool is a computer program.

Claim 19 (Previously presented): The kit of claim 18 wherein the data analysis tool comprises an algorithm adapted to discriminate between the expression profiles of tumours with differing prognoses.

Claim 20 (Previously presented): The kit of claim 16 comprising expression profiles from breast tumour samples with known prognoses and/or expression profiles characteristic of a particular prognosis.

Claim 21 (Cancelled)

Claim 22 (Currently Amended): A kit for assigning a prognosis to a patient with breast cancer, said kit comprising a no more



~~than 500 plurality of~~ nucleic acid binding members capable of specifically binding to nucleic acid expression products of genes of a prognostic set of genes and a detection reagent, wherein the prognostic set includes adenine phosphoribosyltransferase (SEQ ID NO: 1), MCM4 minichromosome maintenance deficient 4 (*S. cerevisiae*) (SEQ ID NO: 2-6), exonuclease 1 (SEQ ID NO: 6-11), Metallothionein 1H-like protein (SEQ ID NO: 12), and clone IMAGE: 5270727 (SEQ ID NO: 13), wherein said binding members are nucleotide primers capable of binding to the nucleic acid expression products of the genes of the prognostic set such that the nucleic acid expression products can be amplified by PCR.

Claim 23 (Currently Amended): A method of producing a nucleic acid expression profile for a breast tumour sample comprising the steps of

(a) isolating nucleic acid expression products from said breast tumour sample;

(b) identifying the expression levels of nucleic acid expression products of a prognostic set of genes, wherein the prognostic set of genes comprises adenine phosphoribosyltransferase (SEQ ID NO: 1), MCM4 minichromosome maintenance deficient 4 (*S. cerevisiae*) (SEQ ID NO: 2-6), exonuclease 1 (SEQ ID NO: 6-11), Metallothionein 1H-like protein (SEQ ID NO: 12), and clone IMAGE: 5270727 (SEQ ID NO: 13); and

(c) producing from the expression levels an expression profile for said breast tumour sample.

Claim 24 (Currently Amended): The method of claim 23, wherein the prognostic set comprises at least 10, 20, 30, 40, 50, 60 or all of the nucleic acids encoded by SEQ ID NOS: 1-309 genes of Table S6.

Claim 25 (Previously presented): The method of claim 23 comprising adding the expression profile to a gene expression



profile database.

Claim 26 (Previously presented): The method of claim 23 further comprising comparing the expression profile with a second expression profile or a plurality of second expression profiles characteristic of a particular prognosis.

Claim 27 (Currently amended): The method of claim 26, comprising the steps of:

(a) isolating nucleic acid expression products from a first breast tumour sample; contacting said expression products with a plurality of binding members capable of specifically and independently binding to expression products of the prognostic set; and creating a first expression profile from the expression levels of the prognostic set in the tumour sample;

(b) isolating nucleic acid expression products from a second breast tumour sample of known prognosis and known NPI status; contacting said expression products with a plurality of binding members capable of specifically and independently binding to expression products of the prognostic set of step (a), so as to create a comparable second expression profile of a breast tumour sample; and

(c) comparing the levels of expression products from said first and second expression profiles to determine the NPI status and prognosis of the first breast tumour sample, wherein comparable alterations in levels of expression products in said first and second samples indicate the prognosis for the patient from which said first sample was obtained ~~match of said first and second expression profiles indicates said~~.

Claims 28-37 (Cancelled)